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Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=5; day=7; hr=12; min=22; sec=32; ms=930;]

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Input Set:

Output Set:

Started: 2009-04-29 19:10:29.018
Finished: 2009-04-29 19:10:33.837
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 819 ms
Total Warnings: 9
Total Errors: 20
No. of SeqIDs Defined: 47
Actual SeqID Count: 47

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
E 257	Invalid sequence data feature in <221> in SEQ ID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44)
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W 213	Artificial or Unknown found in <213> in SEQ ID (46)
E 257	Invalid sequence data feature in <221> in SEQ ID (46)
W 213	Artificial or Unknown found in <213> in SEQ ID (47)
E 257	Invalid sequence data feature in <221> in SEQ ID (47) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> ZHOU, MING-MING
AGGARWAL, ANEEL K.

<120> METHODS OF IDENTIFYING MODULATORS OF BROMODOMAINS

<130> 2459-1-003

<140> 09510314

<141> 2009-04-29

<160> 47

<170> PatentIn version 3.5

<210> 1

<211> 3014

<212> DNA

<213> Homo sapiens

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<210> 2
 <211> 832
 <212> PRT
 <213> Homo sapiens

<400> 2

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				20				25					30		
Pro	Pro	Ala	Pro	Pro	Gln	Gly	Ser	Pro	Cys	Ala	Ala	Ala	Ala	Gly	Gly
				35				40					45		
Ser	Gly	Ala	Cys	Gly	Pro	Ala	Thr	Ala	Val	Ala	Ala	Ala	Gly	Thr	Ala
				50				55					60		
Glu	Gly	Pro	Gly	Gly	Gly	Gly	Ser	Ala	Arg	Ile	Ala	Val	Lys	Lys	Ala
				65				70					75		80
Gln	Leu	Arg	Ser	Ala	Pro	Arg	Ala	Lys	Lys	Leu	Glu	Lys	Leu	Gly	Val
				85				90					95		
Tyr	Ser	Ala	Cys	Lys	Ala	Glu	Glu	Ser	Cys	Lys	Cys	Asn	Gly	Trp	Lys
				100				105					110		
Asn	Pro	Asn	Pro	Ser	Pro	Thr	Pro	Pro	Arg	Ala	Asp	Leu	Gln	Gln	Ile
				115				120					125		
Ile	Val	Ser	Leu	Thr	Glu	Ser	Cys	Arg	Ser	Cys	Ser	His	Ala	Leu	Ala
				130				135					140		
Ala	His	Val	Ser	His	Leu	Glu	Asn	Val	Ser	Glu	Glu	Glu	Met	Asn	Arg
				145				150					155		160

Leu	Leu	Gly	Ile	Val	Leu	Asp	Val	Glu	Tyr	Leu	Phe	Thr	Cys	Val	His	165	170	175	
Lys	Glu	Glu	Asp	Ala	Asp	Thr	Lys	Gln	Val	Tyr	Phe	Tyr	Leu	Phe	Lys	180	185	190	
Leu	Leu	Arg	Lys	Ser	Ile	Leu	Gln	Arg	Gly	Lys	Pro	Val	Val	Glu	Gly	195	200	205	
Ser	Leu	Glu	Lys	Lys	Pro	Pro	Phe	Glu	Lys	Pro	Ser	Ile	Glu	Gln	Gly	210	215	220	
Val	Asn	Asn	Phe	Val	Gln	Tyr	Lys	Phe	Ser	His	Leu	Pro	Ala	Lys	Glu	225	230	235	240
Arg	Gln	Thr	Ile	Val	Glu	Leu	Ala	Lys	Met	Phe	Leu	Asn	Arg	Ile	Asn	245	250	255	
Tyr	Trp	His	Leu	Glu	Ala	Pro	Ser	Gln	Arg	Arg	Leu	Arg	Ser	Pro	Asn	260	265	270	
Asp	Asp	Ile	Ser	Gly	Tyr	Lys	Glu	Asn	Tyr	Thr	Arg	Trp	Leu	Cys	Tyr	275	280	285	
Cys	Asn	Val	Pro	Gln	Phe	Cys	Asp	Ser	Leu	Pro	Arg	Tyr	Glu	Thr	Thr	290	295	300	
Gln	Val	Phe	Gly	Arg	Thr	Leu	Leu	Arg	Ser	Val	Phe	Thr	Val	Met	Arg	305	310	315	320
Arg	Gln	Leu	Leu	Glu	Gln	Ala	Arg	Gln	Glu	Lys	Asp	Lys	Leu	Pro	Leu	325	330	335	
Glu	Lys	Arg	Thr	Leu	Ile	Leu	Thr	His	Phe	Pro	Lys	Phe	Leu	Ser	Met	340	345	350	
Leu	Glu	Glu	Glu	Val	Tyr	Ser	Gln	Asn	Ser	Pro	Ile	Trp	Asp	Gln	Asp	355	360	365	
Phe	Leu	Ser	Ala	Ser	Ser	Arg	Thr	Ser	Gln	Leu	Gly	Ile	Gln	Thr	Val	370	375	380	

Ile Asn Pro Pro Pro Val Ala Gly Thr Ile Ser Tyr Asn Ser Thr Ser
385 390 395 400

Ser Ser Leu Glu Gln Pro Asn Ala Gly Ser Ser Ser Pro Ala Cys Lys
405 410 415

Ala Ser Ser Gly Leu Glu Ala Asn Pro Gly Glu Lys Arg Lys Met Thr
420 425 430

Asp Ser His Val Leu Glu Glu Ala Lys Lys Pro Arg Val Met Gly Asp
435 440 445

Ile Pro Met Glu Leu Ile Asn Glu Val Met Ser Thr Ile Thr Asp Pro
450 455 460

Ala Ala Met Leu Gly Pro Glu Thr Asn Phe Leu Ser Ala His Ser Ala
465 470 475 480

Arg Asp Glu Ala Ala Arg Leu Glu Glu Arg Arg Gly Val Ile Glu Phe
485 490 495

His Val Val Gly Asn Ser Leu Asn Gln Lys Pro Asn Lys Lys Ile Leu
500 505 510

Met Trp Leu Val Gly Leu Gln Asn Val Phe Ser His Gln Leu Pro Arg
515 520 525

Met Pro Lys Glu Tyr Ile Thr Arg Leu Val Phe Asp Pro Lys His Lys
530 535 540

Thr Leu Ala Leu Ile Lys Asp Gly Arg Val Ile Gly Gly Ile Cys Phe
545 550 555 560

Arg Met Phe Pro Ser Gln Gly Phe Thr Glu Ile Val Phe Cys Ala Val
565 570 575

Thr Ser Asn Glu Gln Val Lys Gly Tyr Gly Thr His Leu Met Asn His
580 585 590

Leu Lys Glu Tyr His Ile Lys His Asp Ile Leu Asn Phe Leu Thr Tyr
595 600 605

Ala Asp Glu Tyr Ala Ile Gly Tyr Phe Lys Lys Gln Gly Phe Ser Lys

610

615

620

Glu Ile Lys Ile Pro Lys Thr Lys Tyr Val Gly Tyr Ile Lys Asp Tyr
625 630 635 640

Glu Gly Ala Thr Leu Met Gly Cys Glu Leu Asn Pro Arg Ile Pro Tyr
645 650 655

Thr Glu Phe Ser Val Ile Ile Lys Lys Gln Lys Glu Ile Ile Lys Lys
660 665 670

Leu Ile Glu Arg Lys Gln Ala Gln Ile Arg Lys Val Tyr Pro Gly Leu
675 680 685

Ser Cys Phe Lys Asp Gly Val Arg Gln Ile Pro Ile Glu Ser Ile Pro
690 695 700

Gly Ile Arg Glu Thr Gly Trp Lys Pro Ser Gly Lys Glu Lys Ser Lys
705 710 715 720

Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser Ile Leu
725 730 735

Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu Pro Val
740 745 750

Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Phe Pro Met
755 760 765

Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr Val Ser
770 775 780

Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn Cys Lys
785 790 795 800

Glu Tyr Asn Ala Ala Glu Ser Glu Tyr Tyr Lys Cys Ala Asn Ile Leu
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Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly Leu Ile Asp Lys
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<212> PRT
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<220>
 <223> Description of Artificial Sequence: Synthetic peptide

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 <222> (2)..(4)
 <223> Any amino acid and this region may encompass 2-3 residues

<220>
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 <223> Any amino acid and this region may encompass 5-8 residues

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 <223> Pro, Lys or His

<220>
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 <223> Any amino acid

<220>
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 <223> Tyr, Phe or His

<220>
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<220>
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 <223> Met, Ile or Val

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 Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Asp
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<210> 4
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 <212> PRT
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<220>
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<221> MOD_RES

<222> (6)..(6)

<223> Acetyl-Lys

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<210> 5

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (8)..(8)

<223> Acetyl-Lys

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1 5 10

<210> 6

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

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<220>

<221> MOD_RES

<222> (8)..(8)

<223> Acetyl-Lys

<400> 6

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<210> 7

<211> 110

<212> PRT

<213> Homo sapiens

<400> 7

Ser Lys Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser

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Pro	Val	Lys	Arg	Thr	Glu	Ala	Pro	Gly	Tyr	Tyr	Glu	Val	Ile	Arg	Ser
		35						40					45		

Pro	Met	Asp	Leu	Lys	Thr	Met	Ser	Glu	Arg	Leu	Lys	Asn	Arg	Tyr	Tyr
	50					55						60			

Val	Ser	Lys	Lys	Leu	Phe	Met	Ala	Asp	Leu	Gln	Arg	Val	Phe	Thr	Asn
65					70					75					80

Cys	Lys	Glu	Tyr	Asn	Ala	Pro	Glu	Ser	Glu	Tyr	Tyr	Lys	Cys	Ala	Asn
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<211> 110

<212> PRT

<213> Homo sapiens

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			20					25					30		

Pro	Val	Lys	Lys	Ser	Glu	Ala	Pro	Asp	Tyr	Tyr	Glu	Val	Ile	Arg	Phe
		35						40					45		

Pro	Ile	Asp	Leu	Lys	Thr	Met	Thr	Glu	Arg	Leu	Arg	Ser	Arg	Tyr	Tyr
	50					55					60				

Val	Thr	Arg	Lys	Leu	Phe	Val	Ala	Asp	Leu	Gln	Arg	Val	Ile	Ala	Asn
65					70					75					80

Cys	Arg	Glu	Tyr	Asn	Pro	Pro	Asp	Ser	Glu	Tyr	Cys	Arg	Cys	Ala	Ser
				85					90					95	

Ala Leu Glu Lys Phe Phe Tyr Phe Lys Leu Lys Glu Gly Gly
100 105 110

<210> 9

<211> 109

<212> PRT

<213> Tetrahymena thermophila

<400> 9

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Val Asn Lys Asp Asp Val Pro Asp Tyr Tyr Asp Val Ile Thr Asp Pro
35 40 45

Ile Asp Ile Lys Ala Ile Glu Lys Lys Leu Gln Asn Asn Gln Tyr Val
50 55 60

Asp Lys Asp Gln Phe Ile Lys Asp Val Lys Arg Ile Phe Thr Asn Ala
65 70 75 80

Lys Ile Tyr Asn Gln Pro Asp Thr Ile Tyr Tyr Lys Ala Ala Lys Glu
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Leu Glu Asp Phe Val Glu Pro Tyr Leu Thr Lys Leu Lys
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<210> 10

<211> 109

<212> PRT

<213> Saccharomyces cerevisiae

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20 25 30

Val Asn Lys Glu Glu Val Pro Asp Tyr Tyr Asp Phe Ile Lys Glu Pro
35 40 45

Met Asp Leu Ser Thr Met Glu Ile Lys Leu Glu Ser Asn Lys Tyr Gln

50

55

60

Lys Met Glu Asp Phe Ile Tyr Asp Ala Arg Leu Val Phe Asn Asn Cys
65 70 75 80

Arg Met Tyr Asn Gly Glu Asn Thr Ser Tyr Tyr Lys Tyr Ala Asn Arg
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Leu Glu Lys Phe Phe Asn Asn Lys Val Lys Glu Ile Pro
100 105

<210> 11

<211> 112

<212> PRT

<213> Homo sapiens

<400> 11

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20 25 30

Pro Val Asp Pro Gln Leu Leu Gly Ile Pro Asp Tyr Phe Asp Ile Val
35